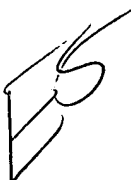


**In the Claims:**

Please amend the Claims as follows.

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12. (Amended) A method for generating a secondary library of scaffold protein sequences comprising:

- 
- a) receiving a library of primary sequences generated utilizing a force field calculation;
  - b) generating a probability distribution table of amino acid residues in a plurality of variant positions from said primary sequences; and
  - c) combining a plurality of said amino acid residues to generate a secondary library of secondary sequences; wherein at least one of said secondary sequences is different from said primary sequences.

13. (Amended) A method according to claim 12, wherein said force field calculation is Self-Consistent Mean Field (SCMF).

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15. (Amended) A method according to claim 14, wherein a Protein Design Automation program is used to recombine said secondary library.



16. (Amended) A method for generating a secondary library of scaffold protein variants comprising:


- a) receiving a library of primary sequences generated utilizing an alignment program;
- b) generating a probability distribution table of amino acid residues in a plurality of variant positions from said primary sequences;
- c) combining a plurality of said amino acid residues to generate a secondary library of secondary sequences, wherein at least one of said secondary sequences is different from said primary sequences; and
- d) computationally ranking said secondary library.

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18. (Amended) A method according to claim 17, wherein a Protein Design Automation program is used to recombine said secondary library.

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24. (Amended) A method according to claim 22 wherein said pooled oligonucleotides are added in amounts that correspond to the frequency of the mutation.

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Please add the following new claims:

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26. (New) A method for generating a secondary library of scaffold protein sequences comprising:

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- a) generating a probability distribution table of amino acid residues in a plurality of variant positions from a force field calculation; and